



**UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office**

Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
-----------------	-------------	----------------------	---------------------

09/357,273 07/20/99 KAUFMAN

R UMV-1584

EXAMINER

000959
LAHIVE & COCKFIELD
28 STATE STREET
BOSTON MA 02109

HM12/0222

KERR, J

ART UNIT

PAPER NUMBER

1633
DATE MAILED:

02/22/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

DEA/FCE-1994

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/357,273	7/20/99	Kaufman et al.	UMV-1584

EXAMINER	
Janet M. Kerr	
ART UNIT	PAPER NUMBER
1633	9

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The communication, filed on 12/14/00, is non-responsive to the prior Office action, mailed 8/22/00, because of the following reason:

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR § 1.821 through 1.825 (see attached Raw Sequence Listing Error Report). Failure to respond to this requirement may result in abandonment of the instant application.

Since the response appears to be *bona fide*, but through an apparent oversight or inadvertence failed to provide a complete response, applicant is required to complete the response within a time limit of one month from the date of this letter or as extended as follows. AN EXTENSION OF THIS TIME LIMIT MAY BE GRANTED UNDER EITHER 37 C.F.R. § 1.136(a) OR (b) UP TO A MAXIMUM OF SIX MONTHS.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. ~~Papers should be faxed to Technical Center 1600 via the~~ PTO Fax Center located in Crystal Mall 1. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989).

The CM1 Fax Center number is either (703)305-3014 or (703)308-4242.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Janet M. Kerr, Ph.D., whose telephone number is (703)305-4055.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Deborah Clark, can be reached at (703)305-4051.

Any inquiry of a general nature or relating to the status of this application should be directed to Patent Analyst, Kimberly Davis, whose telephone number is (703)305-3015 or to the Technical Center receptionist whose telephone number is (703)308-0196.

DEBORAH J. R. CLARK
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Raw Sequence Listing Error Summary

48

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/352,273

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) 2. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1633

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/357,273

DATE: 12/11/2000
 TIME: 16:45:05

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\12112000\I357273.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Kaufman, Randal J.
 4 Tirasophon, Witoon
 5 Welihinda, Ajith A.
 7 <120> TITLE OF INVENTION: Irep, A NOVEL MAMMALIAN PROTEIN AND GENE ENCODING SAME
 9 <130> FILE REFERENCE: UMW-1584
 11 <140> CURRENT APPLICATION NUMBER: US/09/357,273
 12 <141> CURRENT FILING DATE: 1999-07-20
 14 <150> PRIOR APPLICATION NUMBER: 60/093,526
 15 <151> PRIOR FILING DATE: 1998-07-21
 17 <160> NUMBER OF SEQ ID NOS: 14
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 3629
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Artificial Sequence
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (97)..(3027)
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 33 <400> SEQUENCE: 1
 34 ccggctcgac ggctcggatc ccgcctcgtc gtcgtcgcgg cgcgcccggc cgtcctctgt 60
 36 ccgtaccgcc cccggagcca gggccgagtc ctcgcc atg ccg gcc cgg cgg ctg 114
 37 Met Pro Ala Arg Arg Leu
 38 1 5
 40 ctg ctg ctg ctg acg ctg ctg ctg ccc gcc ctc ggg att ttt gga agt 162
 41 Leu Leu Leu Leu Thr Leu Leu Leu Pro Gly Leu Gly Ile Phe Gly Ser
 42 10 15 20
 44 acc agc aca gtg acg ctt cct gaa acc ttg ttg ttt gtg tca acg ctg 210
 45 Thr Ser Thr Val Thr Leu Pro Glu Thr Leu Leu Phe Val Ser Thr Leu
 46 25 30 35
 48 gat gga agt ttg cat gct gtc agc aag agg aca gcc tca atc aaa tgg 258
 49 Asp Gly Ser Leu His Ala Val Ser Lys Arg Thr Gly Ser Ile Lys Trp
 50 40 45 50
 52 act tta aaa gaa gat cca gtc ctg cag gtc cca aca cat gtg gaa gag 306
 53 Thr Leu Lys Glu Asp Pro Val Leu Gln Val Pro Thr His Val Glu Glu
 54 55 60 65 70
 56 cct gcc ttt ctc cca gat cct aat gat gcc agc ctg tat acg ctt gga 354
 57 Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly Ser Leu Tyr Thr Leu Gly
 58 75 80 85
 60 agc aag aat aat gaa gcc ctg acg aaa ctt cct ttt acc atc cca gaa 402
 61 Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu Pro Phe Thr Ile Pro Glu
 62 90 95 100
 64 ttg gtg cag gca tcc coa tgc cga agt tca gat gga atc ctc tac atg 450
 65 Leu Val Gln Ala Ser Pro Cys Arg Ser Ser Asp Gly Ile Leu Tyr Met
 66 105 110 115
 68 ggt aaa aag cag gac atc tgg tat gtt att gac ctc ctg acc gga gag 498

P.5

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/357,273

DATE: 12/11/2000

TIME: 16:45:05

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\12112000\I357273.raw

```

69 Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile Asp Leu Leu Thr Gly Glu
70      120      125      130
72 aag cag cag act ttg tca tcg gcc ttt gca gat agt ctc tgc cca tca 546
73 Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala Asp Ser Leu Cys Pro Ser
74 135      140      145      150
76 acc tct ctt ctg tat ctt ggg cga aca gaa tac acc atc acc atg tac 594
77 Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu Tyr Thr Ile Thr Met Tyr
78      155      160      165
80 gac acc aaa acc cga gag ctc cgg tgg aat gcc acc tac ttt gac tat 642
81 Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn Ala Thr Tyr Phe Asp Tyr
82      170      175      180
84 gcg gcc tca ctg cct gag gac gaa ggg gac tac aag atg tcc cac ttt 690
85 Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp Tyr Lys Met Ser His Phe
86      185      190      195
88 gtg tcc aat ggt gat ggg ctg gtg act gtg gac agt gaa tct ggg 738
89 Val Ser Asn Gly Asp Gly Leu Val Val Thr Val Asp Ser Glu Ser Gly
90      200      205      210
92 gac gtc ctg tgg atc caa aac tac gcc tcc cct gtg gtg gcc ttt tat 786
93 Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser Pro Val Val Ala Phe Tyr
94 215      220      225      230
96 gtc tgg cag cgg gag ggt ctg agg aag gtg atg cac atc aat gtc gct 834
97 Val Trp Gln Arg Glu Gly Leu Arg Lys Val Met His Ile Asn Val Ala
98      235      240      245
100 gtg gag acc ctg cgc tat ctg acc ttc atg tct ggg gag gtg ggg cgc 882
101 Val Glu Thr Leu Arg Tyr Leu Thr Phe Met Ser Gly Glu Val Gly Arg
102      250      255      260
104 atc aca aag tgg aag tac ccg ttc ccc aag gag aca gag gcc aag agc 930
105 Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys Glu Thr Glu Ala Lys Ser
106      265      270      275
108 aag ctg acg ccc act ctg tat gtt ggg aaa tac tct acc agc ctc tat 978
109 Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys Tyr Ser Thr Ser Leu Tyr
110      280      285      290
112 gcc tct ccc tca atg gta cac gag ggg gtt gct gtc gtg ccc cgc ggc 1026
113 Ala Ser Pro Ser Met Val His Glu Gly Val Ala Val Val Pro Arg Gly
114 295      300      305      310
116 agc aca ctt cct ttg ctg gaa ggg ccc cag act gat ggc gtc acc atc 1074
117 Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln Thr Asp Gly Val Thr Ile
118      315      320      325
120 ggg gac aag ggg gag tgt gtg atc acg ccc agc acg gac gtc aag ttt 1122
121 Gly Asp Lys Gly Glu Cys Val Ile Thr Pro Ser Thr Asp Val Lys Phe
122      330      335      340
124 gat ccc gga ctc aaa agc aag aac aag ctc aac tac ttg agg aat tac 1170
125 Asp Pro Gly Leu Lys Ser Lys Asn Lys Leu Asn Tyr Leu Arg Asn Tyr
126      345      350      355
128 tgg ctt ctg ata gga cac cat gaa acc cca ctg tct gcg tct acc aag 1218
129 Trp Leu Leu Ile Gly His His Glu Thr Pro Leu Ser Ala Ser Thr Lys
130      360      365      370
132 atg ctg gag aga ttt ccc aac aat cta ccc aaa cat cgg gaa aat gtg 1266
133 Met Leu Glu Arg Phe Pro Asn Asn Leu Pro Lys His Arg Glu Asn Val

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/357,273

DATE: 12/11/2000

TIME: 16:45:05

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\12112000\I357273.raw

134	375	380	385	390	
136	att cct gct gat tca gag aaa aag agc ttt gag gaa gtt atc aac ctg	1314			
137	Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe Glu Glu Val Ile Asn Leu				
138	395 400 405				
140	gtt gac cag act tca gaa aac gca cct acc acc gtg tct cgg gat gtg	1362			
141	Val Asp Gln Thr Ser Glu Asn Ala Pro Thr Thr Val Ser Arg Asp Val				
142	410 415 420				
144	gag gag aag ccc gcc cat gcc cct gcc cgg ccc gag gcc ccc gta gac	1410			
145	Glu Glu Lys Pro Ala His Ala Pro Ala Arg Pro Glu Ala Pro Val Asp				
146	425 430 435				
148	tcc atg ctt aag gac atg gct acc atc atc ctg agc acc ttc ctg ctg	1458			
149	Ser Met Leu Lys Asp Met Ala Thr Ile Ile Leu Ser Thr Phe Leu Leu				
150	440 445 450				
152	att ggc tgg gtg gcc ttc atc atc acc tat ccc ctg agc atg cat cag	1506			
153	Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr Pro Leu Ser Met His Gln				
154	455 460 465 470				
156	cag cag cag ctc cag cac cag cag ttc cag aag gaa ctg gag aag atc	1554			
157	Gln Gln Gln Leu Gln His Gln Gln Phe Gln Lys Glu Leu Glu Lys Ile				
158	475 480 485				
160	cag ctc ctg cag cag cag cag cag cag ctg ccc ttc cac cca cct gga	1602			
161	Gln Leu Leu Gln Gln Gln Gln Gln Leu Pro Phe His Pro Pro Gly				
162	490 495 500				
164	gac acg tgc cag gac ggc gag ctc ctg gac acg tct ggc cgg tac tca	1650			
165	Asp Thr Ala Gln Asp Gly Glu Leu Leu Asp Thr Ser Gly Pro Tyr Ser				
166	505 510 515				
168	gag agc tgc ggc acc agc agc ccc agc acg tcc ccc agg gcc tcc aac	1698			
169	Glu Ser Ser Gly Thr Ser Ser Pro Ser Thr Ser Pro Arg Ala Ser Asn				
170	520 525 530				
172	cac tgc ctc tgc tcc ggc agc tct gcc tcc aag gct ggc agc agc ccc	1746			
173	His Ser Leu Cys Ser Gly Ser Ser Ala Ser Lys Ala Gly Ser Ser Pro				
174	535 540 545 550				
176	tcc ctg gaa caa gac gat gga gat gag gaa acc agc gtg gtg ata gtt	1794			
177	Ser Leu Glu Gln Asp Asp Gly Asp Glu Glu Thr Ser Val Val Ile Val				
178	555 560 565				
180	ggg aaa att tcc ttc tgt ccc aag gat gtc ctg ggc cat gga gct gag	1842			
181	Gly Lys Ile Ser Phe Cys Pro Lys Asp Val Leu Gly His Gly Ala Glu				
182	570 575 580				
184	ggc aca att gtg tac cgg ggc atg ttt gac aac cgc gac gtg gcc gtg	1890			
185	Gly Thr Ile Val Tyr Arg Gly Met Phe Asp Asn Arg Asp Val Ala Val				
186	585 590 595				
188	aag agg atc ctc ccc gag tgt ttt agc ttc gca gac cgt gag gtc cag	1938			
189	Lys Arg Ile Leu Pro Glu Cys Phe Ser Phe Ala Asp Arg Glu Val Gln				
190	600 605 610				
192	ctg ttg cga gaa tgc gat gag cac ccg aac gtg atc cgc tac ttc tgc	1986			
193	Leu Leu Arg Glu Ser Asp Glu His Pro Asn Val Ile Arg Tyr Phe Cys				
194	615 620 625 630				
196	acg gag aag gac cgg caa ttc cag tac att gcc atc gag ctg tgt gca	2034			
197	Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile Ala Ile Glu Leu Cys Ala				
198	635 640 645				

RECEIVED

DEC 26 2000

TECH CENTER 1600/2500

RAW SEQUENCE LISTING

DATE: 12/11/2000

PATENT APPLICATION: US/09/357,273

TIME: 16:45:05

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\12112000\I357273.raw

```

200 gcc acc ctg caa gag tat gtg gag cag aag gac ttt gcg cat ctc ggc 2082
201 Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys Asp Phe Ala His Leu Gly
202 650 655 660
204 ctg gag ccc atc acc ttg ctg cag cag acc acc tcg ggc ctg gcc cac 2130
205 Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr Thr Ser Gly Leu Ala His
206 665 670 675
208 ctc cac tcc ctc aac atc gtt cac aga qac cta aag cca cac aac atc 2178
209 Leu His Ser Leu Asn Ile Val His Arg Asp Leu Lys Pro His Asn Ile
210 680 685 690
212 ctc ata tcc atg ccc aat gca cac ggc aag atc aag gcc atg atc tcc 2226
213 Leu Ile Ser Met Pro Asn Ala His Gly Lys Ile Lys Ala Met Ile Ser
214 695 700 705 710
216 gac ttt ggc ctc tgc aag aag ctg gca gtg ggc aga cac agt ttc agc 2274
217 Asp Phe Gly Leu Cys Lys Lys Leu Ala Val Gly Arg His Ser Phe Ser
218 715 720 725
220 cgc cga tct ggg gtg cct ggc aca gaa qgc tgg atc gct cca gag atg 2322
221 Arg Arg Ser Gly Val Pro Gly Thr Glu Gly Trp Ile Ala Pro Glu Met
222 730 735 740
224 ctg agc gaa gac tgt aag gag aac cct acc tac acg gtg gac atc ttt 2370
225 Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr Tyr Thr Val Asp Ile Phe
226 745 750 755
228 tct gca ggc tgc gtc ttt tac tac gtg gtc tct gag ggc agc cac cct 2418
229 Ser Ala Gly Cys Val Phe Tyr Tyr Val Val Ser Glu Gly Ser His Pro
230 760 765 770
232 ttt ggc aag tcc ctg cag cgg cag gcc aac atc ctc ctg ggt gcc tgc 2466
233 Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn Ile Leu Leu Gly Ala Cys
234 775 780 785 790
236 agc ctt gac tgc ttg cac cca gag aag cac gaa gac gtc att gca cga 2514
237 Ser Leu Asp Cys Leu His Pro Glu Lys His Glu Asp Val Ile Ala Arg
238 795 800 805
240 gaa ttg ata gag aag atg att gcg atg gat cct cag aaa cgc ccc tca 2562
241 Glu Leu Ile Glu Lys Met Ile Ala Met Asp Pro Gln Lys Arg Pro Ser
242 810 815 820
244 gcg aac gac gtg ctc aaa cac ccg ttc ttc tgg agc cta gag aag cag 2610
245 Ala Asn Asp Val Leu Lys His Pro Phe Phe Trp Ser Leu Glu Lys Gln
246 825 830 835
248 ctc cag ttc ttc cag gac gtg agc gac aga ata gaa aag gaa tcc ctg 2658
249 Leu Gln Phe Phe Gln Asp Val Ser Asp Arg Ile Glu Lys Glu Ser Leu
250 840 845 850
252 gat ggc ccg atc gtg aag cag tta gag aga ggc ggg aga gcc gtg gtg 2706
253 Asp Gly Pro Ile Val Lys Gln Leu Glu Arg Gly Gly Arg Ala Val Val
254 855 860 865 870
256 aag atg gac tgg cgg gag aac atc act gac ccc ctc cag aca gac ctg 2754
257 Lys Met Asp Trp Arg Glu Asn Ile Thr Asp Pro Leu Gln Thr Asp Leu
258 875 880 885
260 cgt aaa ttc agg acc tat aaa ggt ggt tct gtc aga gat ctc ctc cga 2802
261 Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser Val Arg Asp Leu Leu Arg
262 890 895 900
264 gcc atg aga aat aag aag cac cac tac cgg gag ctg cct gca gag gtg 2850

```


RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/357,273

DATE: 12/11/2000

TIME: 16:45:05

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\12112000\I357273.raw

RECEIVED

DEC 26 2000

TECH CENTER 1600/2500

```

265 Ala Met Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Ala Glu Val
266          905          910          915
268 cgg gag acg ctg ggg acc ctc ccc gac gac ttc gtg tgc tac ttc acg 2898
269 Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp Phe Val Cys Tyr Phe Thr
270          920          925          930
272 tot cgc ttc ccc cac ctc ctc gca cac acc tac cgg gcc atg gag ctg 2946
273 Ser Arg Phe Pro His Leu Leu Ala His Thr Tyr Arg Ala Met Glu Leu
274 935          940          945          950
276 tgc agc cac gag aga ctc ttc cag ccc tac tac ttc cac gag ccc cca 2994
277 Cys Ser His Glu Arg Leu Phe Gln Pro Tyr Tyr Phe His Glu Pro Pro
278          955          960          965
280 gag ccc cag ccc cca gtg act cca gac gcc ctc tgagcgaggg cggccccctct 3047
281 Glu Pro Gln Pro Pro Val Thr Pro Asp Ala Leu
282          970          975
284 gttctggttg cccagctgt gactgagggc ctggtcacca caatlaqagc ttgatgcctc 3107
286 cggcctttgc agggagacca ggcctcccaa accaagtgcc ttgagctgcc tgctctgcag 3167
288 cccacagagg acagtgcctga cccaggaag tgggagaagt gcccctcgt gacctacag 3227
290 gaactgggaa gatgctggcc ccaaaagcct tacggtcatg atgtctgcaa aggagggcct 3287
292 cagagacagc gcgagtagca ccccaagcca tctactggat aaacttgctt cagacttttt 3347
294 aaattcctgc ttaatgtcag tctacaggcc ttccaggaag ggagaggag  gaatcgtaca 3407
296 ttttgcctgc gtgctgggac agctaggctg agatgcacca agtacagcct tcactggaga 3467
298 ccggaattga gaggtggggg atgctgagga gggggaggac ggagttcaga ggggtgctgc 3527
300 ctgcagtatg agatttctca ttgatcacag atgtgcccag agtagcccag gtcactgtta 3587
302 actagtgttt ctgcagaggc agcaggagcc agcccggaat tc 3629
305 <210> SEQ ID NO: 2
306 <211> LENGTH: 977
307 <212> TYPE: PRT
308 <213> ORGANISM: Artificial Sequence
W--> 310 <220> FEATURE:
W--> 310 <223> OTHER INFORMATION:
310 <400> SEQUENCE: 2
311 Met Pro Ala Arg Arg Leu Leu Leu Leu Thr Leu Leu Leu Pro Gly
312 1          5          10          15
314 Leu Gly Ile Phe Gly Ser Thr Ser Thr Val Thr Leu Pro Glu Thr Leu
315          20          25          30
317 Leu Phe Val Ser Thr Leu Asp Gly Ser Leu His Ala Val Ser Lys Arg
318          35          40          45
320 Thr Gly Ser Ile Lys Trp Thr Leu Lys Glu Asp Pro Val Leu Gln Val
321          50          55          60
323 Pro Thr His Val Glu Glu Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly
324 65          70          75          80
326 Ser Leu Tyr Thr Leu Gly Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu
327          85          90          95
329 Pro Phe Thr Ile Pro Glu Leu Val Gln Ala Ser Pro Cys Arg Ser Ser
330          100          105          110
332 Asp Gly Ile Leu Tyr Met Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile
333          115          120          125
335 Asp Leu Leu Thr Gly Glu Lys Gln Gln Thr Leu Ser Ala Phe Ala
336          130          135          140

```

→ see item 7 on Ena Summary Sheet

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 12/11/2000

PATENT APPLICATION: US/09/357,273

TIME: 16:45:06

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\12112000\I357273.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:310 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:310 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1023 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:1023 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:1023 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8